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93118

From: Yu, Misook
Sent: Monday, May 05, 2003 9:04 AM
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Subject: 09/851,422

Please search SEQ ID NO:1, 2, and 8. They are all small peptides.

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Phone:_____
Location:_____
Date Picked Up:_____
Date Completed: 5/7/03
Searcher Prep/Review:_____
Clerical:_____
Online time:_____

TYPE OF SEARCH:
NA Sequences:_____
AA Sequences:_____
Structures:_____
Bibliographic:_____
Litigation:_____
Full text:_____
Patent Family:_____
Other:_____

VENDOR/COST (where applic.)
STN:_____
DIALOG:_____
Questel/Orbit:_____
DRLink:_____
Lexis/Nexis:_____
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Other (specify):_____

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FILE COVERS 1907 - 7 May 2003  VOL 138 ISS 19
FILE LAST UPDATED: 6 May 2003  (20030506/ED)

 This file contains CAS Registry Numbers for easy and accurate
 substance identification.


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L1          6019 SEA FILE=REGISTRY ABB=ON  PLU=ON  LVDRATCLR|DRAT|VPHNESE/SQSP
L2            16 SEA FILE=REGISTRY ABB=ON  PLU=ON  L1 AND SQL=< 20
L3            12 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L2


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L3   ANSWER 1 OF 12  HCAPLUS  COPYRIGHT 2003 ACS
ACCESSION NUMBER:         2003:202677  HCAPLUS
DOCUMENT NUMBER:          138:236915
TITLE:                    Engineering of human coagulation factor IX for
                          reduction or elimination of immunogenicity
INVENTOR(S):              Carr, Francis J.; Carter, Graham
PATENT ASSIGNEE(S):       Merck Patent GmbH, Germany
SOURCE:                   PCT Int. Appl., 49 pp.
                          CODEN: PIXXD2
DOCUMENT TYPE:            Patent
LANGUAGE:                 English
FAMILY ACC. NUM. COUNT:   1
PATENT INFORMATION:

     PATENT NO.         KIND  DATE          APPLICATION NO.  DATE
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     WO 2003020764       A2   20030313      WO 2002-EP9717   20020830
         W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
             CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
             GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
             LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH,
             PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ,
             UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU,
             TJ, TM
         RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG,
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CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: EP 2001-121154 A 20010904

AB The authors disclose the engineering of human factor IX to result in a modified protein(s) that are substantially non-immunogenic or less immunogenic than the non-modified counterpart. The engineering of immunogenicity comprises a characterization of epitopes for class II-restricted T-cells.

IT **501118-82-7 501118-83-8 501118-84-9 501118-85-0 501118-86-1**
RL: ADV (Adverse effect, including toxicity); PRP (Properties); BIOL (Biological study)
(engineering of human coagulation factor IX for redn. or elimination of)

L3 ANSWER 2 OF 12 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2003:118086 HCAPLUS
DOCUMENT NUMBER: 138:168794
TITLE: Early detection of mycobacterial disease using peptides
INVENTOR(S): Laal, Suman; Zolla-Pazner, Susan; Belisle, John T.
PATENT ASSIGNEE(S): New York University, USA
SOURCE: PCT Int. Appl., 120 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003012395	A2	20030213	WO 2002-US24297	20020802

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 2001-309185P P 20010802

AB A no. of protein and glycoprotein antigens secreted by Mycobacterium tuberculosis (Mtb) have been identified as "early" Mtb antigens on the basis of early antibodies present in subjects infected with Mtb prior to the development of detectable clin. disease. Epitope-bearing peptide fragments of these early Mtb antigens, in particular of an 88 kDa secreted protein, GlcB (SEQ ID NO:106) and of Mtb antigen MPT51 (SEQ ID NO:107) have been identified. These peptides, variants thereof, peptide multimers thereof that include two or more repeats of one or more of the peptides, and fusion polypeptides that include early Mtb antigenic proteins, peptides or both, are useful in immunoassay methods for early, rapid detection of TB in a subject. Preferred immunoassays detect the antibodies in the subject's urine. Also provided are antigenic compns., kits and methods useful for detecting early Mtb antibodies. The antigenic proteins and peptides are also used in vaccine compns.

IT **496911-39-8 496911-40-1**
RL: PRP (Properties)
(unclaimed sequence; early detection of mycobacterial disease using peptides)

L3 ANSWER 3 OF 12 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:716304 HCAPLUS
DOCUMENT NUMBER: 137:259591
TITLE: System and method for systematic prediction of ligand/receptor activity
INVENTOR(S): Brusic, Vladimir
PATENT ASSIGNEE(S): Kent Ridge Digital Labs, Singapore
SOURCE: PCT Int. Appl., 45 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002072613	A1	20020919	WO 2001-SG49	20010310

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: WO 2001-SG49 20010310

AB The invention concerns a general system and method, for prediction of binding of peptide-like ligands (peptides) to peptide-like receptors (receptors). Specifically this invention uses non-linear prediction models (including, but not limited to, artificial neural networks), sequence data form ligands and their resp. receptors, and known ligand-receptor binding affinities. The representation of ligand-receptor interaction used along with the binding affinity of said interaction is used to train a detg. means in a form of a predictive model. Prediction of binding affinity of a novel (not used for training of a predictive model) ligand-receptor interaction, involving a peptide and a particular receptor, involves the combining of representations of both peptide and receptor and presenting that representation to a previously trained predictive model. The system and method can be used as a single predictive model for detn. of ligand binding to an individual receptor, or to a group of related receptors. This system and method was validated using data on peptide binding to major histocompatibility complex mols. (MHC) and artificial neural networks (ANN).

IT **461387-07-5 461387-29-1 461387-34-8**
RL: PRP (Properties)
(unclaimed sequence; system and method for systematic prediction of ligand/receptor activity)

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 4 OF 12 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:595012 HCAPLUS
DOCUMENT NUMBER: 137:168253
TITLE: Antigenic peptides from G protein-coupled receptors and their antibodies and systems for identifying such antigenic peptides
INVENTOR(S): Burmer, Glenna C.; Roush, Christine L.; Brown, Joseph P.
PATENT ASSIGNEE(S): Lifespan Biosciences, Inc., USA
SOURCE: PCT Int. Appl., 523 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002061087	A2	20020808	WO 2001-US50107	20011219

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 2000-257144P A2 20001219

AB The present invention provides antigenic peptides from G protein-coupled receptors (GPCRs) and antibodies relating thereto, and related systems, methods, compns., and the like, such as diagnostics and medicaments. Where antibodies against a given GPCR are not known, the present invention provides such antibodies, and preferred antigenic sequences for producing such antibodies. Where antibodies against a given GPCR are known, the present invention provides preferred antigenic peptides for producing antibodies that exhibit improved specificity, affinity, or capacity to perform antibody-related actions relative to the known antibodies. Thus, 1600 antigenic peptides are derived from the amino acid sequence of specific GPCRs based on analyses of likely antigen-contg. regions and specificity of those regions for the protein/gene of interest. The specificity of the antigen peptides (.apprx.20 amino acids in length) for antibody generation is detd. using BLAST of several public databases and selecting for at least 3 characteristics selected from the group consisting of (1) at least two consecutive prolines, (2) at least two consecutive serines, (3) at least two consecutive lysines, (4) at least two consecutive arginines, (5) at least two consecutive aspartic acids, (6) at least two consecutive glutamic acids, (7) methionine, (8) tryptophan, and (9) at least five consecutive amino acids comprising no charged amino acids. The present invention also provides improved methods of selecting antigenic peptides from any desired protein or polypeptide, as well as antigenic peptides so produced and antibodies against such antigenic peptides. Kits and assays are provided for the detection of antibodies against a particular GPCR or other target polypeptide in a sample.

IT **444697-38-5**
RL: ANT (Analyte); ARG (Analytical reagent use); BUU (Biological use, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(antigenic peptides from G protein-coupled receptors and their antibodies and systems for identifying such antigenic peptides)

L3 ANSWER 5 OF 12 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:94109 HCAPLUS
DOCUMENT NUMBER: 136:117375
TITLE: Antigenic peptides from Neisseria meningitidis and Neisseria gonorrhoeae
INVENTOR(S): Galeotti, Cesira; Grandi, Guido; Masignani, Vega; Mora, Mariarosa; Pizza, Mariagrazia; Rappuoli, Rino; Ratti, Guilio; Scarlato, Vincenzo; Scarselli, Maria
PATENT ASSIGNEE(S): Chiron S.p.A., Italy
SOURCE: PCT Int. Appl., 974 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent

LANGUAGE: English
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001031019 A2		20010503	WO 2000-IB1661	20001030

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG

PRIORITY APPLN. INFO.: US 1999-PV162616 19991029

AB This invention provides proteins and fragments thereof derived from the bacteria Neisseria meningitidis serotype A, N. meningitidis serotype B, and N. gonorrhoeae. Th protein sequences disclosed in International Application patents WO 1999/57280 and WO 2000/22430 were subjected to computer anal. to predict antigenic peptide fragments, using three algorithms: AMPHI, ANTIGENIC INDEX, and HYDROPHOBICITY. Also provided are nucleic acids encoding for such proteins, polypeptides, and/or fragments, as well as nucleic acids complementary thereto (e.g., antisense nucleic acids). Addnl., this invention provides antibodies which bind to the proteins, polypeptides, and/or fragments. This invention further provides expression vectors useful for making the proteins, polypeptides, and/or fragments, as well as host cells transformed with such vectors. This invention also provides compns. of the protein fragments and/or nucleic acids for use as vaccines, diagnostic reagents, immunogenic compns., and the like. [This abstr. record is the sixth of 8 records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.]

IT **336835-32-6**
RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(amino acid sequence; Neisseria meningitidis and N. gonorrhoeae antigens and the genes encoding them for use as vaccine and diagnostic compns.)

L3 ANSWER 6 OF 12 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:871941 HCAPLUS
DOCUMENT NUMBER: 136:4714
TITLE: Antigenic peptides from Neisseria meningitidis and Neisseria gonorrhoeae
INVENTOR(S): Galeotti, Cesira; Grandi, Guido; Masignani, Vega; Mora, Mariarosa; Pizza, Mariagrazia; Rappuoli, Rino; Ratti, Guilio; Scarlato, Vincenzo; Scarselli, Maria
PATENT ASSIGNEE(S): Chiron S.p.A., Italy
SOURCE: PCT Int. Appl., 974 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001031019 A2		20010503	WO 2000-IB1661	20001030

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG
PRIORITY APPLN. INFO.: US 1999-PV162616 19991029
AB This invention provides proteins and fragments thereof derived from the bacteria Neisseria meningitidis serotype A, N. meningitidis serotype B, and N. gonorrhoeae. Th protein sequences disclosed in International Application patents WO 1999/57280 and WO 2000/22430 were subjected to computer anal. to predict antigenic peptide fragments, using three algorithms: AMPHI, ANTIGENIC INDEX, and HYDROPHOBICITY. Also provided are nucleic acids encoding for such proteins, polypeptides, and/or fragments, as well as nucleic acids complementary thereto (e.g., antisense nucleic acids). Addnl., this invention provides antibodies which bind to the proteins, polypeptides, and/or fragments. This invention further provides expression vectors useful for making the proteins, polypeptides, and/or fragments, as well as host cells transformed with such vectors. This invention also provides compns. of the protein fragments and/or nucleic acids for use as vaccines, diagnostic reagents, immunogenic compns., and the like. [This abstr. is the fourth of 8 records for this codument necessitated by the large no. of index entries required to fully index the document and publication system constraints.]
IT **336835-32-6**
RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(amino acid sequence; Neisseria meningitidis and N. gonorrhoeae antigens and the genes encoding them for use as vaccine and diagnostic compns.)

L3 ANSWER 7 OF 12 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:320112 HCAPLUS
DOCUMENT NUMBER: 134:339530
TITLE: Antigenic peptides from Neisseria meningitidis and Neisseria gonorrhoeae
INVENTOR(S): Galeotti, Cesira; Grandi, Guido; Masignani, Vega; Mora, Mariarosa; Pizza, Mariagrazia; Rappuoli, Rino; Ratti, Guilio; Scarlato, Vincenzo; Scarselli, Maria
PATENT ASSIGNEE(S): Chiron Spa, Italy
SOURCE: PCT Int. Appl., 947 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001031019 A2		20010503	WO 2000-IB1661	20001030

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG
PRIORITY APPLN. INFO.: US 1999-PV162616 19991029
AB This invention provides proteins and fragments thereof derived from the bacteria Neisseria meningitidis serotype A, N. meningitidis serotype B, and N. gonorrhoeae. Th protein sequences disclosed in International Application patents WO 1999/57280 and WO 2000/22430 were subjected to computer anal. to predict antigenic peptide fragments, using three algorithms: AMPHI, ANTIGENIC INDEX, and HYDROPHOBICITY. Also provided are nucleic acids encoding for such proteins, polypeptides, and/or fragments, as well as nucleic acids complementary thereto (e.g., antisense nucleic acids). Addnl., this invention provides antibodies which bind to the

proteins, polypeptides, and/or fragments. This invention further provides expression vectors useful for making the proteins, polypeptides, and/or fragments, as well as host cells transformed with such vectors. This invention also provides compns. of the protein fragments and/or nucleic acids for use as vaccines, diagnostic reagents, immunogenic compns., and the like. [This abstract record is the first of 8 records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.]

IT **336835-32-6**
RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(antigenic peptides from Neisseria meningitidis and Neisseria gonorrhoeae)

L3 ANSWER 8 OF 12 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:241777 HCAPLUS
DOCUMENT NUMBER: 134:247961
TITLE: Cloning and genetic mapping of human ataxia-telangiectasia gene (ATM) and diagnosis of the disease by mutation detection
INVENTOR(S): Shiloh, Yosef; Tagle, Danilo A.; Collins, Francis
PATENT ASSIGNEE(S): The United States of America, Department of Health and Human Services, USA; Ramot University Authority for Applied Research and Industrial Dev.
SOURCE: U.S., 61 pp., Cont.-in-part of U.S. 5,777,093.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 8
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6211336	B1	20010403	US 1998-952127	19980226
US 5756288	A	19980526	US 1995-441822	19950516
US 5728807	A	19980317	US 1995-493092	19950621
US 5777093	A	19980707	US 1995-508836	19950728
WO 9636695	A1	19961121	WO 1996-US7040	19960516

W: AL, AM, AU, BB, BG, BR, CA, CN, CZ, EE, FI, GE, HU, IS, JP, KG, KP, KR, LK, LR, LT, LV, MD, MG, MK, MN, MX, NO, NZ, PL, RO, SG, SI, SK, TR, TT, UA, US, UZ, VN, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.:
US 1995-441822 A2 19950516
US 1995-493092 A2 19950621
US 1995-508836 A2 19950728
WO 1996-US7040 W 19960516

AB This invention provides a sequence and genomic location of ATM gene which assocd. with human ataxia-telangiectasia. The human ATM gene consists of 3056 amino acids and located in the region q22-23 of human chromosome 11. The human ATM gene shares a high sequence homol. with mouse ATM gene provided by this invention. ATM genes has a highly conserved C-terminal region showing high sequence homol. to the catalytic domain of PI-3 kinase indicating that the possible working model of human ATM gene is signal transduction between DNA damage and checkpoint system. Various mutation patterns of the ATM gene is clamed in this invention which causes human ataxia-telangiectasia. The det. and detection of the special mutation pattern of the ATM gene can be used to diagnose ataxia-telangiectasia.

IT **185410-66-6**
RL: PRP (Properties)
(unclaimed sequence; cloning and genetic mapping of human ataxia-telangiectasia gene (ATM) and diagnosis of the disease by

mutation detection)
REFERENCE COUNT: 62 THERE ARE 62 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 9 OF 12 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:688272 HCAPLUS
DOCUMENT NUMBER: 133:280563
TITLE: Human antibodies that bind human IL-12 and methods for producing
INVENTOR(S): Salfeld, Jochen G.; Roguska, Michael; Paskind, Michael; Banerjee, Subhashis; Tracey, Daniel E.; White, Michael; Kaymakcalan, Zehra; Labkovsky, Boris; Sakorafas, Paul; Friedrich, Stuart; Myles, Angela; Veldman, Geertruida M.; Venturini, Amy; Warne, Nicholas W.; Widom, Angela; Elvin, John G.; Duncan, Alexander R.; Derbyshire, Elaine J.; Carmen, Sara; Smith, Stephen; Holtet, Thor Las; Du, Fou Sarah L.
PATENT ASSIGNEE(S): Basf A.-G., Germany; Genetics Institute Inc.; et al.
SOURCE: PCT Int. Appl., 377 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000056772	A1	20000928	WO 2000-US7946	20000324
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
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NZ 513945	A	20010928	NZ 2000-513945	20000324
BR 2000009323	A	20020108	BR 2000-9323	20000324
EP 1175446	A1	20020130	EP 2000-918396	20000324
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
JP 2002542770	T2	20021217	JP 2000-606632	20000324
NO 2001004605	A	20011126	NO 2001-4605	20010921

PRIORITY APPLN. INFO.: US 1999-126603P P 19990325
WO 2000-US7946 W 20000324

AB Human antibodies, preferably recombinant human antibodies, that specifically bind to human interleukin-12 (hIL-12) are disclosed. Preferred antibodies have high affinity for hIL-12 and neutralize hIL-12 activity in vitro and in vivo . An antibody of the invention can be a full-length antibody or an antigen-binding portion thereof. The antibodies, or antibody portions, of the invention are useful for detecting hIL-12 and for inhibiting hIL-12 activity, e.g., in a human subject suffering from a disorder in which hIL-12 activity is detrimental. Nucleic acids, vectors and host cells for expressing the recombinant human antibodies of the invention, and methods of synthesizing the recombinant human antibodies, are also encompassed by the invention.

IT **297740-63-7**
RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(recombinant human antibodies that bind human IL-12 for treatment of autoimmune diseases and inflammatory diseases)

REFERENCE COUNT: 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS

RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 10 OF 12 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1997:72207 HCAPLUS
DOCUMENT NUMBER: 126:87941
TITLE: The human ataxia-telangiectasia gene ATM, the gene product, and novel mutations giving rise to the disease
INVENTOR(S): Shiloh, Yosef; Tagle, Danilo A.; Collins, Francis S.
PATENT ASSIGNEE(S): Ramot-University Authority for Applied Research and Industrial Development, Ltd., Israel; United States Dept. of Health and Human Services; Shiloh, Yosef; Tagle, Danilo A.; Collins, Francis S.
SOURCE: PCT Int. Appl., 126 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 8
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9636695	A1	19961121	WO 1996-US7040	19960516
W: AL, AM, AU, BB, BG, BR, CA, CN, CZ, EE, FI, GE, HU, IS, JP, KG, KP, KR, LK, LR, LT, LV, MD, MG, MK, MN, MX, NO, NZ, PL, RO, SG, SI, SK, TR, TT, UA, US, UZ, VN, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
US 5756288	A	19980526	US 1995-441822	19950516
US 5728807	A	19980317	US 1995-493092	19950621
US 5777093	A	19980707	US 1995-508836	19950728
AU 9658608	A1	19961129	AU 1996-58608	19960516
AU 709009	B2	19990819		
EP 826033	A1	19980304	EP 1996-920237	19960516
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 11506909	T2	19990622	JP 1996-535050	19960516
US 6211336	B1	20010403	US 1998-952127	19980226

PRIORITY APPLN. INFO.:
US 1995-441822 A 19950516
US 1995-493092 A 19950621
US 1995-508836 A 19950728
WO 1996-US7040 W 19960516

AB The human gene designated ATM, mutations of which cause ataxia-telangiectasia, is cloned and characterized. Methods of identifying carriers of ATM alleles giving rise to ataxia telangiectasia are described. The gene was cloned after mapping to the 11q22-23 region, using YACs covering the interval D11S384-D11S1818 to obtain the full-length gene. Heterogeneity in the 5'-region of the gene appeared to arise from differential splicing of the transcript. The protein has a no. of sequence motifs that indicate a role in signal transduction and it is suggested to be a phosphatidylinositol-3-kinase. Sequencing of genes from ataxia-telangiectasia patients identified 34 new mutations in the ATM genes. Methods of detecting these mutations, including restriction endonuclease fingerprinting are described.

IT **185410-66-6**
RL: BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(amino acid sequence, antigenic peptide of ataxia-telangiectasia protein; human ataxia-telangiectasia gene ATM, gene product, and novel mutations giving rise to disease)

L3 ANSWER 11 OF 12 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1994:407302 HCAPLUS
DOCUMENT NUMBER: 121:7302
TITLE: Antibodies specific for a hemostatic protein and their use in the isolation of the protein free of proteolysis products for use in hemostatic compositions
INVENTOR(S): Van Mourik, Jan Aart; Van, Mourik Jan Aart
PATENT ASSIGNEE(S): Stichting Centraal Laboratorium van de Bloedtransfusiedienst van het Nederlandse Rode Kruis, Neth.
SOURCE: PCT Int. Appl., 32 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9405692	A1	19940317	WO 1993-NL174	19930826
W: AU, CA, JP, US				
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
EP 658168	A1	19950621	EP 1993-921129	19930826
EP 658168	B1	20001115		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
JP 08500833	T2	19960130	JP 1993-507069	19930826
AU 678987	B2	19970619	AU 1993-48359	19930826
AU 9348359	A1	19940329		
AT 197590	E	20001215	AT 1993-921129	19930826
ES 2152953	T3	20010216	ES 1993-921129	19930826
US 5932706	A	19990803	US 1997-797842	19970210

PRIORITY APPLN. INFO.: EP 1992-202615 A 19920827
WO 1993-NL174 W 19930826

AB A method for the generation of Ca2+-independent antibodies against blood coagulation factors uses an antibody selection strategy based on small peptides that are target sequences for limited proteolysis. These antibodies distinguish between intact and cleaved species of the hemostatic protein, provide novel tools for the isolation of intact hemostatic proteins. The absence of cleavage products usually assocd. with side effects or reduced efficacy means that the intact proteins may serve as improved agents in therapeutic compns. for the treatment of hemostatic disorders. A Ca2+-independent monoclonal antibody to human factor IX was prepd. by std. methods using the primary activation site peptide Q139-D154 as the antigen with hybridomas screened for Ca2+-independent binding to factor IX. The use of the immobilized monoclonal antibodies to purify factor IX and its ability to differentiate proteolysis products and the intact protein are described. Similar expts. are described for protein S.

IT **155569-46-3**
RL: BIOL (Biological study)
(monoclonal antibodies to, for prepn. of protein free of cleavage products)

L3 ANSWER 12 OF 12 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1993:531522 HCAPLUS
DOCUMENT NUMBER: 119:131522
TITLE: Serine protease derived-polypeptides, anti-peptide antibodies, and systems and therapeutic methods for inhibiting coagulation
INVENTOR(S): Griffin, John H.; Mesters, Rolf M.
PATENT ASSIGNEE(S): Scripps Research Institute, USA
SOURCE: PCT Int. Appl., 149 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9309804	A1	19930527	WO 1992-US10242	19921118
W: CA, JP				
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, SE				
US 5679639	A	19971021	US 1994-295411	19940822
US 5968751	A	19991019	US 1997-955471	19971021

PRIORITY APPLN. INFO.: US 1991-793989 19911118
US 1994-295411 19940822

AB Peptides and anti-peptide antibodies are disclosed which can inhibit serine protease activity. In particular, peptides and anti-peptide antibodies derived from the blood coagulation serine proteases Factor VIIa, Factor IXa, Factor Xa, Factor XIa, thrombin, and plasma kallikrein are described that are capable of inhibiting coagulation. The peptides and antibodies are useful in methods and systems for inhibiting serine proteases, end esp. for inhibiting blood coagulation processes mediated by serine proteases in vitro or in a human patient. Prodn. of polyclonal and monoclonal antibodies to protein C fragments is described; activity of the peptides and antibodies of the invention (peptide sequences included) is demonstrated in a variety of coagulation-related assays.

IT **149754-55-2**, Blood-coagulation factor IX fragment
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(amino acid sequence of and anticoagulant activity of)

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STRUCTURE FILE UPDATES: 6 MAY 2003 HIGHEST RN 511508-58-0
DICTIONARY FILE UPDATES: 6 MAY 2003 HIGHEST RN 511508-58-0

TSCA INFORMATION NOW CURRENT THROUGH JANUARY 6, 2003

Please note that search-term pricing does apply when conducting SmartSELECT searches.

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. See HELP PROPERTIES for more information. See STNote 27, Searching Properties in the CAS Registry File, for complete details:
http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf

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=> d .seq l2 tot

L2 ANSWER 1 OF 16 REGISTRY COPYRIGHT 2003 ACS
RN 501118-86-1 REGISTRY
CN L-Lysine, L-prolyl-L-leucyl-L-valyl-L-.alpha.-aspartyl-L-arginyl-L-alanyl-L-threonyl-L-cysteinyl-L-leucyl-L-arginyl-L-seryl-L-threonyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 102: PN: WO03020764 TABLE: 1 claimed sequence
SQL 13
SQL 13

SEQ 1 PLVDRATCLR STK
=========
HITS AT: 2-10

REFERENCE 1: 138:236915

L2 ANSWER 2 OF 16 REGISTRY COPYRIGHT 2003 ACS
RN 501118-85-0 REGISTRY
CN L-Threonine, L-valyl-L-prolyl-L-leucyl-L-valyl-L-.alpha.-aspartyl-L-arginyl-L-alanyl-L-threonyl-L-cysteinyl-L-leucyl-L-arginyl-L-seryl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 101: PN: WO03020764 TABLE: 1 claimed sequence
SQL 13
SQL 13

SEQ 1 VPLVDRATCL RST
======== =
HITS AT: 3-11

REFERENCE 1: 138:236915

L2 ANSWER 3 OF 16 REGISTRY COPYRIGHT 2003 ACS
RN 501118-84-9 REGISTRY
CN L-Arginine, L-leucyl-L-arginyl-L-valyl-L-prolyl-L-leucyl-L-valyl-L-.alpha.-aspartyl-L-arginyl-L-alanyl-L-threonyl-L-cysteinyl-L-leucyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 100: PN: WO03020764 TABLE: 1 claimed sequence
SQL 13
SQL 13

SEQ 1 LRVPLVDRAT CLR
====== ===
HITS AT: 5-13

REFERENCE 1: 138:236915

L2 ANSWER 4 OF 16 REGISTRY COPYRIGHT 2003 ACS
RN 501118-83-8 REGISTRY
CN L-Cysteine, L-glutaminyl-L-tyrosyl-L-leucyl-L-arginyl-L-valyl-L-prolyl-L-leucyl-L-valyl-L-.alpha.-aspartyl-L-arginyl-L-alanyl-L-threonyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 99: PN: WO03020764 TABLE: 1 claimed sequence
SQL 13
SQL 13

SEQ 1 QYLRVPLVDR ATC
== ==
HITS AT: 9-12

REFERENCE 1: 138:236915

L2 ANSWER 5 OF 16 REGISTRY COPYRIGHT 2003 ACS
RN 501118-82-7 REGISTRY
CN L-Threonine, L-leucyl-L-glutaminyl-L-tyrosyl-L-leucyl-L-arginyl-L-valyl-L-prolyl-L-leucyl-L-valyl-L-.alpha.-aspartyl-L-arginyl-L-alanyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 98: PN: WO03020764 TABLE: 1 claimed sequence
SQL 13
SQL 13

SEQ 1 LQYLRVPLVD RAT
= ===
HITS AT: 10-13

REFERENCE 1: 138:236915

L2 ANSWER 6 OF 16 REGISTRY COPYRIGHT 2003 ACS
RN 496911-40-1 REGISTRY
CN L-Leucine, L-methionyl-L-.alpha.-glutamyl-L-.alpha.-aspartyl-L-arginyl-L-alanyl-L-threonyl-L-leucyl-L-arginyl-L-isoleucyl-L-seryl-L-seryl-L-glutaminyl- (9CI) (CA INDEX NAME)
SQL 13
SQL 13

SEQ 1 MEDRATLRIS SQL
====
HITS AT: 3-6

REFERENCE 1: 138:168794

L2 ANSWER 7 OF 16 REGISTRY COPYRIGHT 2003 ACS
RN 496911-39-8 REGISTRY
CN L-Leucine, L-isoleucyl-L-histidyl-L-.alpha.-aspartyl-L-valyl-L-alanyl-L-leucyl-L-methionyl-L-.alpha.-glutamyl-L-.alpha.-aspartyl-L-arginyl-L-alanyl-L-threonyl- (9CI) (CA INDEX NAME)
SQL 13
SQL 13

SEQ 1 IHDVALMEDR ATL
== ==
HITS AT: 9-12

REFERENCE 1: 138:168794

L2 ANSWER 8 OF 16 REGISTRY COPYRIGHT 2003 ACS
RN 461387-34-8 REGISTRY
CN L-Valine, L-.alpha.-glutamyl-L-seryl-L-seryl-L-phenylalanyl-L-.alpha.-aspartyl-L-tyrosyl-L-tyrosyl-L-phenylalanyl-L-.alpha.-aspartyl-L-tyrosyl-L-phenylalanyl-L-.alpha.-aspartyl-L-arginyl-L-alanyl-L-threonyl-L-tyrosyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 90: PN: WO02072613 FIGURE: 16 unclaimed sequence
SQL 17
SQL 17

SEQ 1 ESSFDYYFDY FDRATYV
====
HITS AT: 12-15

REFERENCE 1: 137:259591

L2 ANSWER 9 OF 16 REGISTRY COPYRIGHT 2003 ACS

RN 461387-29-1 REGISTRY
CN Glycine, L-tryptophyl-L-prolyl-L-arginyl-L-phenylalanyl-L-.alpha.-aspartyl-L-tyrosyl-L-seryl-L-tyrosyl-L-.alpha.-aspartyl-L-tyrosyl-L-phenylalanyl-L-.alpha.-aspartyl-L-arginyl-L-alanyl-L-threonyl-L-tyrosyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 85: PN: WO02072613 FIGURE: 16 unclaimed sequence
SQL 17
SQL 17

SEQ 1 WPRFDYSYDY FDRATYG
====
HITS AT: 12-15

REFERENCE 1: 137:259591

L2 ANSWER 10 OF 16 REGISTRY COPYRIGHT 2003 ACS
RN 461387-07-5 REGISTRY
CN Glycine, L-.alpha.-glutamyl-L-seryl-L-seryl-L-phenylalanyl-L-.alpha.-aspartyl-L-tyrosyl-L-tyrosyl-L-phenylalanyl-L-.alpha.-aspartyl-L-tyrosyl-L-phenylalanyl-L-.alpha.-aspartyl-L-arginyl-L-alanyl-L-threonyl-L-tyrosyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 37: PN: WO02072613 FIGURE: 12 unclaimed sequence
SQL 17
SQL 17

SEQ 1 ESSFDYYFDY FDRATYG
====
HITS AT: 12-15

REFERENCE 1: 137:259591

L2 ANSWER 11 OF 16 REGISTRY COPYRIGHT 2003 ACS
RN 444697-38-5 REGISTRY
CN L-Glutamic acid, glycyl-L-.alpha.-glutamyl-L-.alpha.-glutamyl-L-arginylglycyl-L-phenylalanyl-L-prolyl-L-prolyl-L-.alpha.-aspartyl-L-arginyl-L-alanyl-L-threonyl-L-prolyl-L-leucyl-L-leucyl-L-glutaminyl-L-threonyl-L-alanyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 149: PN: WO02061087 SEQID: 950 claimed protein
SQL 19
SQL 19

SEQ 1 GEERGFPPDR ATPLLQTAE
== ==
HITS AT: 9-12

REFERENCE 1: 137:168253

L2 ANSWER 12 OF 16 REGISTRY COPYRIGHT 2003 ACS
RN 336835-32-6 REGISTRY
CN L-Threonine, L-seryl-L-isoleucylglycyl-L-.alpha.-aspartyl-L-arginyl-L-alanyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 209: PN: WO0131019 PAGE: 406 claimed protein
CN 4636: PN: WO0131019 PAGE: 702 claimed protein
SQL 7
SQL 7

SEQ 1 SIGDRAT
====
HITS AT: 4-7

REFERENCE 1: 136:117375

REFERENCE 2: 136:4714

REFERENCE 3: 134:339530

L2 ANSWER 13 OF 16 REGISTRY COPYRIGHT 2003 ACS
RN 297740-63-7 REGISTRY
CN L-Leucine, L-glutaminyl-L-seryl-L-tyrosyl-L-.alpha.-aspartyl-L-arginyl-L-alanyl-L-threonyl-L-histidyl-L-prolyl-L-alanyl-L-leucyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 497: PN: WO0056772 SEQID: 573 claimed sequence
SQL 12
SQL 12

SEQ 1 QSYDRATHPA LL
====
HITS AT: 4-7

REFERENCE 1: 133:280563

L2 ANSWER 14 OF 16 REGISTRY COPYRIGHT 2003 ACS
RN 185410-66-6 REGISTRY
CN L-Phenylalanine, L-cysteinyl-L-arginyl-L-glutaminyl-L-leucyl-L-.alpha.-glutamyl-L-histidyl-L-.alpha.-aspartyl-L-arginyl-L-alanyl-L-threonyl-L-.alpha.-glutamyl-L-arginyl-L-lysyl-L-lysyl-L-.alpha.-glutamyl-L-valyl-L-.alpha.-aspartyl-L-lysyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 26: PN: US6211336 SEQID: 16 unclaimed sequence
SQL 19
SQL 19

SEQ 1 CRQLEHDRAT ERKKEVDKF
====
HITS AT: 7-10

REFERENCE 1: 134:247961

REFERENCE 2: 126:87941

L2 ANSWER 15 OF 16 REGISTRY COPYRIGHT 2003 ACS
RN 155569-46-3 REGISTRY
CN L-Threonine, L-alanyl-L-leucyl-L-valyl-L-leucyl-L-glutaminyl-L-tyrosyl-L-leucyl-L-arginyl-L-valyl-L-prolyl-L-leucyl-L-valyl-L-.alpha.-aspartyl-L-arginyl-L-alanyl- (9CI) (CA INDEX NAME)
SQL 16
SQL 16

SEQ 1 ALVLQYLRVP LVDRAT
====
HITS AT: 13-16

REFERENCE 1: 121:7302

L2 ANSWER 16 OF 16 REGISTRY COPYRIGHT 2003 ACS
RN 149754-55-2 REGISTRY
CN L-Threonine, L-leucyl-L-valyl-L-leucyl-L-glutaminyl-L-tyrosyl-L-leucyl-L-arginyl-L-valyl-L-prolyl-L-leucyl-L-valyl-L-.alpha.-aspartyl-L-arginyl-L-alanyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN Blood-coagulation factor IX fragment

SQL 15
SQL 15

SEQ 1 LVLQYLRVPL VDRAT
====

HITS AT: 12-15

REFERENCE 1: 119:131522

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L2            16 SEA FILE=REGISTRY ABB=ON  PLU=ON  L1 AND SQL=< 20
L3            12 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L2
L4             7 SEA FILE=REGISTRY ABB=ON  PLU=ON  VPHNESE/SQSP
L6             7 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L4 NOT L3


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L6   ANSWER 1 OF 7  HCAPLUS  COPYRIGHT 2003 ACS
ACCESSION NUMBER:         2003:18945  HCAPLUS
DOCUMENT NUMBER:          138:67676
TITLE:                    Generation and initial analysis of more than 15,000
                          full-length human and mouse cDNA sequences
AUTHOR(S):                Strausberg, Robert L.; Feingold, Elise A.; Grouse,
                          Lynette H.; Derge, Jeffery G.; Klausner, Richard D.;
                          Collins, Francis S.; Wagner, Lukas; Shenmen, Carolyn
                          M.; Schuler, Gregory D.; Altschul, Stephen F.;
                          Zeeberg, Barry; Buetow, Kenneth H.; Schaefer, Carl F.;
                          Bhat, Narayan K.; Hopkins, Ralph F.; Jordan, Heather;
                          Moore, Troy; Max, Steve I.; Wang, Jun; Hsieh,
                          Florence; Diatchenko, Luda; Marusina, Kate; Farmer,
                          Andrew A.; Rubin, Gerald M.; Hong, Ling; Stapleton,
                          Mark; Soares, M. Bento; Bonaldo, Maria F.; Casavant,
                          Tom L.; Scheetz, Todd E.; Brownstein, Michael J.;
                          Usdin, Ted B.; Toshiyuki, Shiraki; Carninci, Piero;
                          Prange, Christa; Raha, Sam S.; Loquellano, Naomi A.;
                          Peters, Garrick J.; Abramson, Rick D.; Mullahy, Sara
                          J.; Bosak, Stephanie A.; McEwan, Paul J.; McKernan,
                          Kevin J.; Malek, Joel A.; Gunaratne, Preethi H.;
                          Richards, Stephen; Worley, Kim C.; Hale, Sarah;
```

Garcia, Angela M.; Gay, Laura J.; Hulyk, Stephen W.; Villalon, Debbie K.; Muzny, Donna M.; Sodergren, Erica J.; Lu, Xiuhua; Gibbs, Richard A.; Fahey, Jessica; Helton, Erin; Ketteman, Mark; Madan, Anuradha; Rodrigues, Stephanie; Sanchez, Amy; Whiting, Michelle; Madan, Anup; Young, Alice C.; Shevchenko, Yuriy; Bouffard, Gerard G.; Blakesley, Robert W.; Touchman, Jeffrey W.; Green, Eric D.; Dickson, Mark C.; Rodriguez, Alex C.; Grimwood, Jane; Schmutz, Jeremy; Myers, Richard M.; Butterfield, Yaron S. N.; Krzywinski, Martin I.; Skalska, Ursula; Smailus, Duane E.; Schnerch, Angelique; Schein, Jacqueline E.; Jones, Steven J. M.; Marra, Marco A.

CORPORATE SOURCE: National Cancer Institute, NIH, Bethesda, MD, 20892-2580, USA

SOURCE: Proceedings of the National Academy of Sciences of the United States of America (2002), 99(26), 16899-16903
CODEN: PNASA6; ISSN: 0027-8424

PUBLISHER: National Academy of Sciences

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The National Institutes of Health Mammalian Gene Collection (MGC) Program is a multiinstitutional effort to identify and sequence a cDNA clone contg. a complete ORF for each human and mouse gene. ESTs were generated from libraries enriched for full-length cDNAs and analyzed to identify candidate full-ORF clones, which then were sequenced to high accuracy. The MGC has currently sequenced and verified the full ORF for a nonredundant set of >9000 human and >6000 mouse genes. Candidate full-ORF clones for an addnl. 7800 human and 3500 mouse genes also have been identified. All MGC sequences and clones are available without restriction through public databases and clone distribution networks. [This abstr. record is one of eleven records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT **480726-59-8**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; generation and initial anal. of more than 15,000 full-length human and mouse cDNA sequences)

REFERENCE COUNT: 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 2 OF 7 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2003:8443 HCAPLUS

DOCUMENT NUMBER: 138:164530

TITLE: Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

AUTHOR(S): Okazaki, Y.; Furuno, M.; Kasukawa, T.; Adachi, J.; Bono, H.; Kondo, S.; Nikaido, I.; Osato, N.; Saito, R.; Suzuki, H.; Yamanaka, I.; Kiyosawa, H.; Yagi, K.; Tomaru, Y.; Hasegawa, Y.; Nogami, A.; Schoenbach, C.; Gojobori, T.; Baldarelli, R.; Hill, D. P.; Bult, C.; Hume, D. A.; Quackenbush, J.; Schriml, L. M.; Kanapin, A.; Matsuda, H.; Batalov, S.; Beisel, K. W.; Blake, J. A.; Bradt, D.; Brusic, V.; Chothia, C.; Corbani, L. E.; Cousins, S.; Dalla, E.; Dragani, T. A.; Fletcher, C. F.; Forrest, A.; Frazer, K. S.; Gaasterland, T.; Gariboldi, M.; Gissi, C.; Godzik, A.; Gough, J.; Grimmond, S.; Gustincich, S.; Hirokawa, N.; Jackson, I. J.; Jarvis, E. D.; Kanai, A.; Kawaji, H.; Kawasawa, Y.; Kedzierski, R. M.; King, B. L.; Konagaya, A.; Kurochkin, I. V.; Lee, Y.; Lenhard, B.; Lyons, P. A.; Maglott, D. R.; Maltais, L.; Marchionni, L.; McKenzie,

L.; Miki, H.; Nagashima, T.; Numata, K.; Okido, T.; Pavan, W. J.; Pertea, G.; Pesole, G.; Petrovsky, N.; Pillai, R.; Pontius, J. U.; Qi, D.; Ramachandran, S.; Ravasi, T.; Reed, J. C.; Reed, D. J.; Reid, J.; Ring, B. Z.; Ringwald, M.; Sandelin, A.; Schneider, C.; Semple, C. A. M.; Setou, M.; Shimada, K.; Sultana, R.; Takenaka, Y.; Taylor, M. S.; Teasdale, R. D.; Tomita, M.; Verardo, R.; Wagner, L.; Wahlestedt, C.; Wang, Y.; Watanabe, Y.; Wells, C.; Wilming, L. G.; Wynshaw-Boris, A.; Yanagisawa, M.; Yang, I.; Yang, L.; Yuan, Z.; Zavolan, M.; Zhu, Y.; Zimmer, A.; Carninci, P.; Hayatsu, N.; Hirozane-Kishikawa, T.; Konno, H.; Nakamura, M.; Sakazume, N.; Sato, K.; Shiraki, T.; Waki, K.; Kawai, J.; Aizawa, K.; Arakawa, T.; Fukuda, S.; Hara, A.; Hashizume, W.; Imotani, K.; Ishii, Y.; Itoh, M.; Kagawa, I.; Miyazaki, A.; Sakai, K.; Sasaki, D.; Shibata, K.; Shinagawa, A.; Yasunishi, A.; Yoshino, M.; Waterston, R.; Lander, E. S.; Rogers, J.; Birney, E.; Hayashizaki, Y.

CORPORATE SOURCE: Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan

SOURCE: Nature (London, United Kingdom) (2002), 420(6915), 563-573
CODEN: NATUAS; ISSN: 0028-0836

PUBLISHER: Nature Publishing Group

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Only a small proportion of the mouse genome is transcribed into mature mRNA transcripts. There is an international collaborative effort to identify all full-length mRNA transcripts from the mouse, and to ensure that each is represented in a phys. collection of clones. The manual annotation of 60,770 full-length mouse cDNA sequences is now reported. These are clustered into 33,409 'transcriptional units', contributing 90.1% of a newly established mouse transcriptome database. Of these transcriptional units, 4258 are new protein-coding and 11,665 are new non-coding messages, indicating that non-coding RNA is a major component of the transcriptome. Forty-one percent of all transcriptional units showed evidence of alternative splicing. In protein-coding transcripts, 79% of splice variations altered the protein product. Whole-transcriptome analyses resulted in the identification of 2431 sense-antisense pairs. The present work, completely supported by phys. clones, provides the most comprehensive survey of a mammalian transcriptome so far, and is a valuable resource for functional genomics. The cDNA sequences are deposited in GenBank/EMBL/DDBJ under accession nos. AK002213-AK021412, AK027261-AK054560, AK075567-AK090394, and AK117103-AK117104. [This abstr. record is one of thirty records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT **493650-09-2**, GenBank BAC40412
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; anal. of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs)

L6 ANSWER 3 OF 7 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2002:921224 HCAPLUS

DOCUMENT NUMBER: 138:84295

TITLE: Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

AUTHOR(S): Okazaki, Y.; Furuno, M.; Kasukawa, T.; Adachi, J.; Bono, H.; Kondo, S.; Nikaido, I.; Osato, N.; Saito,

R.; Suzuki, H.; Yamanaka, I.; Kiyosawa, H.; Yagi, K.; Tomaru, Y.; Hasegawa, Y.; Nogami, A.; Schoenbach, C.; Gojobori, T.; Baldarelli, R.; Hill, D. P.; Bult, C.; Hume, D. A.; Quackenbush, J.; Schriml, L. M.; Kanapin, A.; Matsuda, H.; Batalov, S.; Beisel, K. W.; Blake, J. A.; Bradt, D.; Brusic, V.; Chothia, C.; Corbani, L. E.; Cousins, S.; Dalla, E.; Dragani, T. A.; Fletcher, C. F.; Forrest, A.; Frazer, K. S.; Gaasterland, T.; Gariboldi, M.; Gissi, C.; Godzik, A.; Gough, J.; Grimmond, S.; Gustincich, S.; Hirokawa, N.; Jackson, I. J.; Jarvis, E. D.; Kanai, A.; Kawaji, H.; Kawasawa, Y.; Kedzierski, R. M.; King, B. L.; Konagaya, A.; Kurochkin, I. V.; Lee, Y.; Lenhard, B.; Lyons, P. A.; Maglott, D. R.; Maltais, L.; Marchionni, L.; McKenzie, L.; Miki, H.; Nagashima, T.; Numata, K.; Okido, T.; Pavan, W. J.; Pertea, G.; Pesole, G.; Petrovsky, N.; Pillai, R.; Pontius, J. U.; Qi, D.; Ramachandran, S.; Ravasi, T.; Reed, J. C.; Reed, D. J.; Reid, J.; Ring, B. Z.; Ringwald, M.; Sandelin, A.; Schneider, C.; Semple, C. A. M.; Setou, M.; Shimada, K.; Sultana, R.; Takenaka, Y.; Taylor, M. S.; Teasdale, R. D.; Tomita, M.; Verardo, R.; Wagner, L.; Wahlestedt, C.; Wang, Y.; Watanabe, Y.; Wells, C.; Wilming, L. G.; Wynshaw-Boris, A.; Yanagisawa, M.; Yang, I.; Yang, L.; Yuan, Z.; Zavolan, M.; Zhu, Y.; Zimmer, A.; Carninci, P.; Hayatsu, N.; Hirozane-Kishikawa, T.; Konno, H.; Nakamura, M.; Sakazume, N.; Sato, K.; Shiraki, T.; Waki, K.; Kawai, J.; Aizawa, K.; Arakawa, T.; Fukuda, S.; Hara, A.; Hashizume, W.; Imotani, K.; Ishii, Y.; Itoh, M.; Kagawa, I.; Miyazaki, A.; Sakai, K.; Sasaki, D.; Shibata, K.; Shinagawa, A.; Yasunishi, A.; Yoshino, M.; Waterston, R.; Lander, E. S.; Rogers, J.; Birney, E.; Hayashizaki, Y.

CORPORATE SOURCE: Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan

SOURCE: Nature (London, United Kingdom) (2002), 420(6915), 563-573
CODEN: NATUAS; ISSN: 0028-0836

PUBLISHER: Nature Publishing Group

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Only a small proportion of the mouse genome is transcribed into mature mRNA transcripts. There is an international collaborative effort to identify all full-length mRNA transcripts from the mouse, and to ensure that each is represented in a phys. collection of clones. The manual annotation of 60,770 full-length mouse cDNA sequences is now reported. These are clustered into 33,409 'transcriptional units', contributing 90.1% of a newly established mouse transcriptome database. Of these transcriptional units, 4258 are new protein-coding and 11,665 are new non-coding messages, indicating that non-coding RNA is a major component of the transcriptome. Forty-one percent of all transcriptional units showed evidence of alternative splicing. In protein-coding transcripts, 79% of splice variations altered the protein product. Whole-transcriptome analyses resulted in the identification of 2431 sense-antisense pairs. The present work, completely supported by phys. clones, provides the most comprehensive survey of a mammalian transcriptome so far, and is a valuable resource for functional genomics. The cDNA sequences are deposited in GenBank/EMBL/DDBJ under accession nos. AK002213-AK021412, AK027261-AK054560, AK075567-AK090394, and AK117103-AK117104. [This abstr. record is one of thirty records for this document necessitated by the large no. of index entries required to fully index the document and

publication system constraints.].

IT **326048-50-4**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; anal. of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs)

REFERENCE COUNT: 53 THERE ARE 53 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 4 OF 7 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:872086 HCAPLUS
DOCUMENT NUMBER: 136:32768
TITLE: Nucleic acids and their encoded polypeptides from human tissues
INVENTOR(S): Tang, Y. Tom; Liu, Chenghua; Drmanac, Radoje T.
PATENT ASSIGNEE(S): Hyseq, Inc., USA
SOURCE: PCT Int. Appl., 831 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 76
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001088088	A2	20011122	WO 2001-XB14827	20010516
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
WO 2001088088	A2	20011122	WO 2001-US14827	20010516
WO 2001088088	A3	20021031		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				

PRIORITY APPLN. INFO.: US 2000-577408 A 20000518
WO 2001-US14827 W 20010516

AB The present invention provides a collection or library of 8051 nucleic acid contig sequences assembled from expressed sequence tag or cDNA libraries isolated mainly by sequencing by hybridization (SBH), std. PCR, Sanger sequencing techniques, and in some cases, sequences obtained form one or more public databases. The cDNA libraries are from human tissue sources and nearest neighbor sequence homologies are provided. The invention also relates to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. [This abstr. record is one of four records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT **375901-52-3**
RL: ANT (Analyte); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)

(amino acid sequence; nucleic acids and their encoded polypeptides from human tissues)

L6 ANSWER 5 OF 7 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:781083 HCAPLUS
DOCUMENT NUMBER: 135:353783
TITLE: Human nucleic acids and their encoded polypeptides
INVENTOR(S): Tang, Y. Tom; Liu, Chenghua; Drmanac, Radoje T.
PATENT ASSIGNEE(S): Hyseq, Inc., USA
SOURCE: PCT Int. Appl., 765 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 76
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001079449	A2	20011025	WO 2001-US8656	20010416
WO 2001079449	A3	20020328		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 2001050872	A5	20011030	AU 2001-50872	20010416

PRIORITY APPLN. INFO.:
US 2000-552929 A 20000418
US 2001-770160 A 20010126
WO 2001-US8656 W 20010416

AB The present invention provides 5497 novel nucleic acids, 5497 novel polypeptide sequences encoded by these nucleic acids, and their uses for diagnostic, therapeutic, and research purposes. A collection or library of the novel nucleic acid sequences were assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization, and in some cases, sequences obtained from one or more public databases. Contigs were assembled using the EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling addnl. sequences from different databases that belong to this assemblage. [This abstr. record is one of two records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT **368940-85-6P**
RL: ANT (Analyte); BOC (Biological occurrence); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation); USES (Uses)
(amino acid sequence; human nucleic acids and their encoded polypeptides)

L6 ANSWER 6 OF 7 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:208827 HCAPLUS
DOCUMENT NUMBER: 134:203316
TITLE: Functional annotation of a full-length mouse cDNA collection
AUTHOR(S): Kawai, J.; Shinagawa, A.; Shibata, K.; Yoshino, M.; Itoh, M.; Ishii, Y.; Arakawa, T.; Hara, A.; Fukunishi, Y.; Konno, H.; Adachi, J.; Fukuda, S.; Aizawa, K.; Izawa, M.; Nishi, K.; Kiyosawa, H.; Kondo, S.; Yamanaka, I.; Saito, T.; Okazaki, Y.; Gojobori, T.;

Bono, H.; Kasukawa, T.; Saito, R.; Kadota, K.; Matsuda, H.; Ashburner, M.; Batalov, S.; Casavant, T.; Fleischmann, W.; Gaasterland, T.; Gissi, C.; King, B.; Kochiwa, H.; Kuehl, P.; Lewis, S.; Matsuo, Y.; Nikaido, I.; Pesole, G.; Quackenbush, J.; Schriml, L. M.; Staubli, F.; Suzuki, R.; Tomita, M.; Wagner, L.; Washio, T.; Sakai, K.; Okido, T.; Furuno, M.; Aono, H.; Baldarelli, R.; Barsh, G.; Blake, J.; Boffelli, D.; Bojunga, N.; Carninci, P.; de Bonaldo, M. F.; Brownstein, M. J.; Bult, C.; Fletcher, C.; Fujita, M.; Gariboldi, M.; Gustincich, S.; Hill, D.; Hofmann, M.; Hume, D. A.; Kamiya, M.; Lee, N. H.; Lyons, P.; Marchionni, L.; Mashima, J.; Mazzarelli, J.; Mombaerts, P.; Nordone, P.; Ring, B.; Ringwald, M.; Rodriquez, I.; Sakamoto, N.; Sasaki, H.; Sato, K.; Schonbach, C.; Seya, T.; Shibata, Y.; Storch, K.-F.; Suzuki, H.; Toyo-oka, K.; Wang, K. H.; Weitz, C.; Whittaker, C.; Wilming, L.; Wynshaw-Boris, A.; Yoshida, K.; Hasegawa, Y.; Kawaji, H.; Kohtsuki, S.

CORPORATE SOURCE: The RIKEN Genome Exploration Res. Group Phase II Team, Lab. Genome Exploration Res. Group, RIKEN Genomic Sciences Center (GSC), Yokohama Inst., Yokohama, Kanagawa, 230-0045, Japan; The FANTOM Consortium

SOURCE: Nature (London) (2001), 409(6821), 685-690
CODEN: NATUAS; ISSN: 0028-0836

PUBLISHER: Nature Publishing Group

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The RIKEN Mouse Gene Encyclopaedia Project, a systematic approach to detg. the full coding potential of the mouse genome, involves collection and sequencing of full-length cDNAs and phys. mapping of the corresponding genes to the mouse genome. An international functional annotation meeting (FANTOM) was organized to annotate the first 21,076 cDNAs to be analyzed in this project. This report describes the first RIKEN clone collection, which is one of the largest described for any organism. Anal. of these cDNAs extends known gene families and identifies new ones. The sequences are deposited into GenBank with Accession nos. AK002213-AK021412 and AK027261-AK027262. Information about these clones is available at RIKEN (http://www.gsc.riken.go.jp/e/FANTOM/viewer/) and Mouse Genome Informatics (http://www.informatics.jax.org and mirror sites). [This abstr. record is the second of 7 records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.]

IT **326048-50-4**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; functional annotation of a full-length mouse cDNA collection)

L6 ANSWER 7 OF 7 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1997:698834 HCAPLUS

DOCUMENT NUMBER: 128:19757

TITLE: Structure of cDNAs encoding human eukaryotic initiation factor 3 subunits. Possible roles in RNA binding and macromolecular assembly

AUTHOR(S): Asano, Katsura; Vornlocher, Hans-Peter; Richter-Cook, Nancy J.; Merrick, William C.; Hinnebusch, Alan G.; Hershey, John W. B.

CORPORATE SOURCE: Department of Biological Chemistry, School of Medicine, University of California, Davis, CA, 95616, USA

SOURCE: Journal of Biological Chemistry (1997), 272(43), 27042-27052

CODEN: JBCHA3; ISSN: 0021-9258
PUBLISHER: American Society for Biochemistry and Molecular Biology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The mammalian translation initiation factor 3 (eIF3), is a multiprotein complex of .apprx.600 kDa that binds to the 40 S ribosome and promotes the binding of methionyl-tRNAi and mRNA. The cDNAs encoding 5 of the 10 subunits, namely eIF3-p170, -p116, -p110, -p48, and -p36, have been isolated previously. Here we report the cloning and characterization of human cDNAs encoding the major RNA binding subunit, eIF3-p66, and two addnl. subunits, eIF3-p47 and eIF3-p40. Each of these proteins is present in immunoppts. formed with affinity-purified anti-eIF3-p170 antibodies. Human eIF3-p66 shares 64% sequence identity with a hypothetical Caenorhabditis elegans protein, presumably the p66 homolog. Deletion analyses of recombinant derivs. of eIF3-p66 show that the RNA-binding domain lies within an N-terminal 71-amino acid region rich in lysine and arginine. The N-terminal regions of human eIF3-p40 and eIF3-p47 are related to each other and to 17 other eukaryotic proteins, including murine Mov-34, a subunit of the 26 S proteasome. Phylogenetic analyses of the 19 related protein sequences, called the Mov-34 family, distinguish five major subgroups, where eIF3-p40, eIF3-p47, and Mov-34 are each found in a different subgroup. The subunit compn. of eIF3 appears to be highly conserved in Drosophila melanogaster, C. elegans, and Arabidopsis thaliana, whereas only 5 homologs of the 10 subunits of mammalian eIF3 are encoded in S. cerevisiae.

IT **199455-60-2**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; structure of cDNAs encoding human eukaryotic initiation factor 3 subunits and roles in RNA binding and macromol. assembly)

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DICTIONARY FILE UPDATES: 6 MAY 2003 HIGHEST RN 511508-58-0

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Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. See HELP PROPERTIES for more information. See STNote 27, Searching Properties in the CAS Registry File, for complete details:
http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf

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=> d .seq l4 tot

L4   ANSWER 1 OF 7  REGISTRY  COPYRIGHT 2003 ACS
RN   493650-09-2  REGISTRY
CN   GenBank BAC40412 (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   GenBank BAC40412 (Translated from: GenBank AK088537)
SQL  361

SEQ    101 VILASIVDSY ERRNEGAARV IGTLLGTVDK HSVEVTNCFS VPHNESEDEV
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HITS AT:   141-147

REFERENCE   1:  138:164530

L4   ANSWER 2 OF 7  REGISTRY  COPYRIGHT 2003 ACS
RN   481276-54-4  REGISTRY
CN   GenBank BAC04577 (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   GenBank BAC04577 (Translated from: GenBank AK095574)
SQL  350

SEQ    101 RRNEGAARVI GTLLGTVDKH SVEVTNCFSV PHNESEDEVA VDMEFAKNMY
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HITS AT:   130-136

L4   ANSWER 3 OF 7  REGISTRY  COPYRIGHT 2003 ACS
RN   480726-59-8  REGISTRY
CN   Eukaryotic translation initiation factor 3 (human clone MGC:8365
     IMAGE:2819946 47-kilodalton subunit 5) (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   GenBank AAH00490
CN   GenBank AAH00490 (Translated from: GenBank BC000490)
SQL  357

SEQ    101 SIVDSYERRN EGAARVIGTL LGTVDKHSVE VTNCFSVPHN ESEDEVAVDM
                                               ==== ===
HITS AT:   137-143

**RELATED SEQUENCES AVAILABLE WITH SEQLINK**

REFERENCE   1:  138:67676

L4   ANSWER 4 OF 7  REGISTRY  COPYRIGHT 2003 ACS
RN   375901-52-3  REGISTRY
CN   Protein (human clone WO0188088-SEQID-8636 fragment) (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   585: PN: WO0188088 SEQID: 8636 claimed protein
NTE
-----------------------------------------------------------------------
 type            ------ location ------         description
-----------------------------------------------------------------------
uncommon         Aaa-187         -         -
uncommon         Aaa-335         -         -
-----------------------------------------------------------------------
SQL  444

SEQ    201 VEVTNCFSVP HNESEDEVAV DMEFAKNMYE TGIKKVSPNK LILGWYATGH
                  == =====
HITS AT:   209-215

REFERENCE   1:  136:32768
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L4 ANSWER 5 OF 7 REGISTRY COPYRIGHT 2003 ACS
RN 368940-85-6 REGISTRY
CN Protein (human clone WO0179449-SEQID-7186 fragment) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1001: PN: WO0179449 SEQID: 1689 claimed sequence
NTE

type	------ location ------		description
uncommon	Und-187	-	-
uncommon	Und-335	-	-

SQL 444

SEQ 201 VEVTNCFSVP HNESEDEVAV DMEFAKNMYE TGIKKVSPNK LILGWYATGH
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HITS AT: 209-215

REFERENCE 1: 135:353783

L4 ANSWER 6 OF 7 REGISTRY COPYRIGHT 2003 ACS
RN 326048-50-4 REGISTRY
CN Protein (mouse strain C57BL/6J clone 0610037M02 361-amino acid) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AK002778-derived protein GI 12833012
SQL 361

SEQ 101 VILASIVDSY ERRNEGAARV IGTLLGTVDK HSVEVTNCFS VPHNESEDEV
=======
HITS AT: 141-147

REFERENCE 1: 138:84295

REFERENCE 2: 134:203316

L4 ANSWER 7 OF 7 REGISTRY COPYRIGHT 2003 ACS
RN 199455-60-2 REGISTRY
CN Initiation factor (protein formation) eIF-3 (human clone pBSp47-17 eIF-3 subunit p47) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank U94855-derived protein GI 2055431
SQL 357

SEQ 101 SIVDSYERRN EGAARVIGTL LGTVDKHSVE VTNCFSVPHN ESEDEVAVDM
==== ===
HITS AT: 137-143

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 128:19757